
(TM)

Release 3.1A John F. Collins, Biocomputing Research Unit.
Copyright (c) 1993-1998 University of Edinburgh, U.K.
Distribution rights by Oxford Molecular Ltd

MPearch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu Aug 6 14:06:36 1998; MasPar time 11.35 Seconds

Tabular output not generated. 781.822 Million cell updates/sec

Title: >US-08-813-323A-1

Description: (324-566) from US08813323A.pap (3 of 3)

Sequence: 1 SOAEKLKELDKIRPFQNW.....YIKDDTIFIKIVDTSDLPD 243

Scoring table: PAM 150
Gap 11

Searched: 120441 seqs, 36531193 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: pir56

Statistics: 1:pir1 2:pir2 3:pir3 4:pir4 5:nrl3d

Mean 45.997; Variance 110.625; scale 0.416

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	1764	100.0	567	2	I49272	CD40 receptor-associat	3.34e-278
2	1754	99.4	568	2	A55960	CD40 receptor-associat	1.93e-276
3	1754	99.4	568	2	A55649	TNFR-associated prote	1.93e-276
4	1747	99.0	543	2	I53498	CD40-associated prote	3.29e-275
5	811	46.0	501	2	I51512	TNF receptor associat	3.24e-112
6	793	45.0	501	2	S6163	tumor necrosis factor	3.84e-109
7	730	41.4	416	2	B55649	TNFR-associated prote	2.05e-98
8	728	41.3	409	2	A54750	TNF receptor associat	4.48e-98
9	437	24.8	470	2	I38026	MLN 62 protein - huma	1.59e-49
10	164	9.3	760	2	A40195	meprin A (EC 3.4.24.1	7.39e-08
11	151	8.6	748	2	S24134	endopeptidase 2 (EC 3	3.80e-06
12	135	7.7	746	1	HRHDA	meprin A (EC 3.4.24.1	4.05e-04
13	132	7.5	700	1	HRHMB	meprin A (EC 3.4.24.1	9.47e-04
14	128	7.3	283	2	A60364	tropomyosin - migrato	2.90e-03
15	121	6.9	668	2	A42908	meprin A (EC 3.4.24.1	1.98e-02
16	119	6.7	704	2	A48040	meprin beta chain pre	3.39e-02
17	116	6.6	285	2	A25561	tropomyosin II, muscl	7.52e-02
18	114	6.5	284	2	A45488	body-wall muscle trop	1.27e-01
19	114	6.5	284	2	S66320	tropomyosin, fast mus	1.27e-01
20	113	6.4	245	2	C34787	tropomyosin 3 alpha,	1.65e-01
21	113	6.4	248	2	C39816	tropomyosin 5a, fibro	1.65e-01
22	113	6.4	248	2	D39816	tropomyosin 5b, fibro	1.65e-01
23	113	6.4	251	2	B34787	tropomyosin 2 alpha,	1.65e-01

24	113	6.4	535	2	S74703	hypothetical protein	1.65e-01
25	113	6.4	4096	2	A57099	DNA-activated protein	1.65e-01
26	111	6.3	847	2	A53800	mixed-lineage protein	2.78e-01
27	111	6.3	1060	2	S63993	acrosomal protein AZ1	2.78e-01
28	109	6.2	214	2	I40303	outer membrane lipopr	4.63e-01
29	109	6.2	227	2	S05585	tropomyosin - human	4.63e-01
30	110	6.2	284	2	S38381	tropomyosin - Califor	3.59e-01
31	107	6.1	243	2	S55467	tropomyosin isoform -	7.70e-01
32	107	6.1	280	2	A22165	tropomyosin alpha cha	7.70e-01
33	107	6.1	281	2	A34787	tropomyosin 1 alpha,	7.70e-01
34	107	6.1	284	5	2TMAB	tropomyosin alpha cha	7.70e-01
35	107	6.1	284	1	2MRSA	tropomyosin alpha cha	7.70e-01
36	107	6.1	284	5	2TMAA	tropomyosin alpha cha	7.70e-01
37	107	6.1	284	2	A25825	tropomyosin alpha cha	7.70e-01
38	107	6.1	284	2	B27407	tropomyosin alpha cha	7.70e-01
39	107	6.1	284	2	S24972	tropomyosin alpha cha	7.70e-01
40	107	6.1	284	2	A27674	tropomyosin 3, fibrob	7.70e-01
41	107	6.1	284	2	A39816	tropomyosin 2, fibrob	7.70e-01
42	107	6.1	284	2	A60597	tropomyosin 3, fibrob	7.70e-01
43	107	6.1	284	2	B39816	myosin heavy chain, f	7.70e-01
44	107	6.1	676	2	S00084	myosin heavy chain, f	7.70e-01
45	108	6.1	1947	1	S05697	myosin heavy chain C	5.98e-01

ALIGNMENTS

RESULT	1
ENTRY	I49272
TITLE	#type complete
ORGANISM	CD40 receptor-associated factor 1 - mouse
DATE	#formal_name Mus musculus #common_name house mouse
	15-Mar-1996 #sequence_revision 15-Mar-1996 #text_change
	28-Feb-1997
ACCESSIONS	I49272
REFERENCE	A55960
#authors	Cheng, G.; Cleary, A.M.; Ye, Z.S.; Hong, D.I.; Lederman, S.; Baltimore, D.
#journal	Science (1995) 267:1494-1498
#title	Involvement of CRAPI, a relative of TRAF, in CD40 signaling.
#cross-references	MOID:95184010
#accession	I49272
#status	preliminary
#molecule_type	mRNA
#residues	1-567
#label	RES
#cross-references	EMBL:U21050; NID:g719292; PID:g719293
GENETICS	
#gene	CRAPI
KEYWORDS	zinc finger
SUMMARY	#length 567 #molecular-weight 64263 #checksum 4919

Query Match	100.0%	Score 1764; DB 2; Length 567;
Best Local Similarity	100.0%;	Pred. No. 3.34e-278;
Matches	243; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
Db	324	SOAEKLKELDKIRPFQNW
QY	324	SOAEKLKELDKIRPFQNW
Db	384	LSRHDTLSVHDRLADMDLR
QY	384	LSRHDTLSVHDRLADMDLR
Db	444	FYTGFGYKMCARYLNDG
QY	444	FYTGFGYKMCARYLNDG
Db	504	RHLGDAFKPDPNSSFK
QY	504	RHLGDAFKPDPNSSFK
Db	564	LPD 566
QY	564	LPD 566

```

RESULT 2
ENTRY CD40 receptor-associated factor 1 - human
TITLE #formal_name Homo sapiens #common_name man
ORGANISM 15-Mar-1996 #sequence_revision 15-Mar-1996 #text_change
DATE 15-Mar-1996

ACCESSIONS A55960
REFERENCE Cheng, G.; Cleary, A.M.; Ye, Z.S.; Hong, D.I.; Lederman, S.; Baltimore, D.
#journal Science (1995) 267:1494-1498
#title Involvement of CRAF1, a relative of TRAF, in CD40 signaling.
#cross-references MUID:95184010
#accession A55960
#status preliminary
#residues 1-568 #label RES
#cross-references EMBL:U21092; NID:726087; PID:726088

GENETICS
#gene CRAF1
#molecule_type mRNA
#length 568 #molecular-weight 64459 #checksum 8765
SUMMARY
Query Match 99.4%; Score 1754; DB 2; Length 568;
Best Local Similarity 99.2%; Pred. No. 1.93e-276;
Matches 241; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 325 SOAEKLEKDEIRPFQNWEEADSMKSSVESLQNRVTELESVDKSGQVARNITGLLESQ 384
QY 324 SOAEKLEKDEIRPFQNWEEADSMKSSVESLQNRVTELESVDKSGQVARNITGLLESQ 383
Db 385 LSRHDOMLSVHDRLADMDLRFQVLETASVNGVLIWKIRYKRRKQEAVMGKTLISYQ 444
QY 384 LSRHDOMLSVHDRLADMDLRFQVLETASVNGVLIWKIRYKRRKQEAVMGKTLISYQ 443
Db 445 FYTGFGYKMCARYLNGDGMKGTHLSLFFVIMRGEYDALLPWPFPKQKVTLMMDQSS 504
QY 444 FYTGFGYKMCARYLNGDGMKGTHLSLFFVIMRGEYDALLPWPFPKQKVTLMMDQSS 503
Db 505 RRHLDGAFKDPNNSPKPTGEMNTASGCPVFAQTIVLENGYIYKDDTIFIKVIIVDTSD 564
QY 504 RRHLDGAFKDPNNSPKPTGEMNTASGCPVFAQTIVLENGYIYKDDTIFIKVIIVDTSD 563
Db 565 LPD 567
QY 564 LPD 566

RESULT 3
ENTRY TNFR-associated protein LAP1 - human
TITLE CD40-binding protein
ALTERNATE_NAMES #formal_name Homo sapiens #common_name man
ORGANISM 23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change
DATE 10-Sep-1997

ACCESSIONS A55649
REFERENCE Mosialos, G.; Birkenbach, M.; Yalamanchili, R.; VanArsdale, T.; Ware, C.; Kieff, E.
#journal Cell (1995) 80:389-399
#title The Epstein-Barr virus transforming protein LMP1 engages signaling proteins for the tumor necrosis factor receptor family.
#accession A55649
#status nucleic acid sequence not shown
#molecule_type mRNA
#residues 1-568 #label MOS
#cross-references GB:U19260; NID:9675459; PID:9675460
REFERENCE A55135
#authors Hu, H.M.; O'Rourke, K.; Boguski, M.S.; Dixit, V.M.
#journal J. Biol. Chem. (1994) 269:30069-30072
#title A novel ring finger protein interacts with the cytoplasmic

```

```

#accession A55135
#status nucleic acid sequence not shown
#molecule_type mRNA
#residues 1-133,135-404,'G',406-568 #label HUA
#cross-references GB:U15637; NID:g595910; PID:g595911
KEYWORDS coiled coil
FEATURE
53-91
SUMMARY
#region RING finger motif
#length 568 #molecular-weight 64490 #checksum 8660

Query Match 99.4%; Score 1754; DB 2; Length 568;
Best Local Similarity 99.2%; Pred. No. 1.93e-276;
Matches 241; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 325 SOAEKLEKDEIRPFQNWEEADSMKSSVESLQNRVTELESVDKSGQVARNITGLLESQ 384
QY 324 SOAEKLEKDEIRPFQNWEEADSMKSSVESLQNRVTELESVDKSGQVARNITGLLESQ 383
Db 385 LSRHDOMLSVHDRLADMDLRFQVLETASVNGVLIWKIRYKRRKQEAVMGKTLISYQ 444
QY 384 LSRHDOMLSVHDRLADMDLRFQVLETASVNGVLIWKIRYKRRKQEAVMGKTLISYQ 443
Db 445 FYTGFGYKMCARYLNGDGMKGTHLSLFFVIMRGEYDALLPWPFPKQKVTLMMDQSS 504
QY 444 FYTGFGYKMCARYLNGDGMKGTHLSLFFVIMRGEYDALLPWPFPKQKVTLMMDQSS 503
Db 505 RRHLDGAFKDPNNSPKPTGEMNTASGCPVFAQTIVLENGYIYKDDTIFIKVIIVDTSD 564
QY 504 RRHLDGAFKDPNNSPKPTGEMNTASGCPVFAQTIVLENGYIYKDDTIFIKVIIVDTSD 563
Db 565 LPD 567
QY 564 LPD 566

RESULT 4
ENTRY CD40-associated protein - human
TITLE #formal_name Homo sapiens #common_name man
ORGANISM 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
DATE 28-Feb-1997

ACCESSIONS I53498
REFERENCE Sato, T.; Irie, S.; Reed, J.C.
#authors FEBS Lett. (1995) 358:113-118
#journal A novel member of the TRAF family of putative signal
#title transducing proteins binds to the cytosolic domain of CD40.
#cross-references MUID:95129692
#accession I53498
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues 1-543 #label RES
#cross-references GB:I38509; NID:g695357; PID:g695358
GENETICS
#gene CAP-1
#length 543 #molecular-weight 61719 #checksum 5192
SUMMARY
Query Match 99.0%; Score 1747; DB 2; Length 543;
Best Local Similarity 98.8%; Pred. No. 3.29e-275;
Matches 240; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 300 SOAEKLEKDEIRPFQNWEEADSMKSSVESLQNRVTELESVDKSGQVARNITGLLESQ 359
QY 324 SOAEKLEKDEIRPFQNWEEADSMKSSVESLQNRVTELESVDKSGQVARNITGLLESQ 383
Db 360 LSRHDOMLSVHDRLADMDLRFQVLETASVNGVLIWKIRYKRRKQEAVMGKTLISYQ 419
QY 384 LSRHDOMLSVHDRLADMDLRFQVLETASVNGVLIWKIRYKRRKQEAVMGKTLISYQ 443
Db 420 FYTGFGYKMCARYLNGDGMKGTHLSLFFVIMRGEYDALLPWPFPKQKVTLMMDQSS 479
QY 444 FYTGFGYKMCARYLNGDGMKGTHLSLFFVIMRGEYDALLPWPFPKQKVTLMMDQSS 503

```

```

Db 480 RRHLGDAFRPDPNSSFKKPTGEMNIASGCPVFVAQTVLNGTYIKDPTIFIKVIVTSD 539
|||||
QY 504 RRHLGDAFRPDPNSSFKKPTGEMNIASGCPVFVAQTVLNGTYIKDPTIFIKVIVTSD 563
Db 540 LPD 542
|||
QY 564 LPD 566

RESULT 5
ENTRY TNF receptor associated factor 2 - mouse
TITLE #Formal_name Mus musculus #common_name house mouse
ORGANISM 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change
DATE 28-Feb-1997
ACCESSIONS I61512 #type complete
REFERENCE A54750
#authors Rothe, M.; Wong, S.C.; Henzel, W.J.; Goeddel, D.V.
#journal Cell (1994) 78:681-692
#title A novel family of putative signal transducers associated with
the cytoplasmic domain of the 75 kDa tumor necrosis factor
receptor.
#cross-references MUID:94349371
#accession I61512
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues 1-501 #label RES
#cross-references GB:L35303; NID:g532620; PID:g532621
GENETICS
#gene TRAF2
SUMMARY #length 501 #molecular_weight 56026 #checksum 9899
Query Match 46.0%; Score 811; DB 2; Length 501;
Best Local Similarity 52.7%; Pred. No. 3.24e-112;
Matches 98; Conservative 51; Mismatches 35; Indels 2; Gaps 2;

Db 317 LSNKVOQLERSIGLKDLAMADLEQKVSELVSYDGVFIWKISDFTRKRQEAAGRTPAI 376
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
QY 380 LESQLSRHQDTLSVHDIRLADMDLRFQVLEATSYNGVLKIWDYKRKRQEAAGVTKLSL 439
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
Db 377 FSPAFTSYGYKMCRLVRYLNGDGTGRGTHLSLFFVWVKGNPDALLQWPFNQKVTMLLD 436
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
QY 440 YSQPFTYFGYKMCARVYLNLDGDKGTHLSLFFVIMRGEDYDALLPWPFPKQKVTMLMD 499
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
Db 437 H-NNREHVIDAFRPDVTSSSFORPVSMDNIASGCPFLCPVKMKAKNSIYVRDDAIFIKAI 495
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
QY 500 QGSSRHLGDAFRPDPNSSFKKPTGEMNIASGCPVFVAQTVLNGTYIKDPTIFIKVIVTSD 558
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
Db 496 VDLTGL 501
|||
QY 559 VDTSDL 564

RESULT 6
ENTRY TNF receptor associated factor 2 - human
TITLE TNF receptor-associated protein
ALTERNATE_NAMES #Formal_name Homo sapiens #common_name man
ORGANISM 10-Oct-1995 #sequence_revision 01-Dec-1995 #text_change
DATE 10-Sep-1997
ACCESSIONS S56163; S58925; S58926
REFERENCE S56163
#authors Song, H.Y.; Donner, D.B.
#journal Biochem. J. (1995) 309:825-829
#title Association of a RING finger protein with the cytoplasmic
domain of the human type-2 tumour necrosis factor receptor.
#accession S56163
#molecule_type mRNA
#residues 1-501 #label SON
#cross-references EMBL:U12597
REFERENCE S58925
#authors Song, H.Y.; Donner, D.

```



```

KEYWORDS      homology
FEATURE       hydrolase; metalloproteinase; transmembrane protein; zinc
1-33          #domain signal sequence #status experimental #label SIG\
34-77         #domain propeptide #status experimental #label PRO\
78-760        #product meprin A alpha chain #status experimental
              #label MAT\
87-273        #domain astacin homology #label AST\
276-445       #domain MAM homology #label MAM\
167,171,177,226 #binding_site zinc (His, His, Tyr) #status
              predicted\
168           #active_site Glu #status predicted
SUMMARY       #length 760 #molecular-weight 85702 #checksum 4733

Query Match      9.3%; Score 164; DB 2; Length 760;
Best Local Similarity 30.0%; Pred. No. 7.39e-08;
Matches 27; Conservative 25; Mismatches 34; Indels 4; Gaps 4;

Db 447 VWTIRNISQILENTVKGDKL-V-SPRYNSE-GYGVGVTLYPNGRITNSGLGLAFHLY 503
:| | | : : : : | | | : : : : | | | : : : : | | | : : : : | | | :
QY 418 IWKIRYKRRKQEAVMGKTLISYQPTGYGFKMCAVYLVNGDMGKTHLSLFFVIM 477
:| | | : : : : | | | : : : : | | | : : : : | | | : : : : | | | :
Db 504 SGDNDALEWPNVQNAIMTLDQEDARN 533
:| | | : : : : | | | : : : : | | | : : : : | | | : : : : | | | :
QY 478 RGEYDALLPWFQKQVTLM-LMDQGSRRH 506
:| | | : : : : | | | : : : : | | | : : : : | | | : : : : | | | :

RESULT 11
ENTRY   S24134      #type complete
TITLE   endopeptidase 2 (EC 3.4.24.-) - rat
ALTERNATE_NAMES endopeptidase 24.18
ORGANISM #formal_name Rattus norvegicus #common_name Norway rat
DATE     02-Dec-1993 #sequence_revision 01-Sep-1995 #text_change
20-Mar-1998
ACCESSIONS S24134
REFERENCE  S24134
#authors   Corbell, D.; Gaudoux, F.; Wainwright, S.; Ingram, J.; Kenny,
          A.J.; Boileau, G.; Crine, P.
#journal   FEBS Lett. (1992) 309:203-208
#title     Molecular cloning of the alpha-subunit of rat
          endopeptidase-24.18 (endopeptidase-2) and co-localization
          with endopeptidase-24.11 in rat kidney by in situ
          hybridization.
#cross-references MIM:92371675
#accession S24134
#status    preliminary
#molecule_type mRNA
#residues  1-748 #label COR
CLASSIFICATION #superfamily meprin A; astacin homology; EGF homology; MAM
              homology
KEYWORDS      hydrolase; metalloproteinase; zinc
FEATURE       #domain astacin homology #label AST\
76-262        #domain MAM homology #label MAM\
265-434       #binding_site zinc (His) #status predicted\
155,160,166   #active_site Glu #status predicted
157           #length 748 #molecular-weight 85138 #checksum 2333
SUMMARY

Query Match      8.6%; Score 151; DB 2; Length 748;
Best Local Similarity 28.9%; Pred. No. 3.80e-06;
Matches 26; Conservative 23; Mismatches 37; Indels 4; Gaps 4;

Db 436 VWTIRNISQILENTVKGDKL-V-SPRYNSE-GYGVGVTLYPNGRITNSGYLGLAFHLY 492
:| | | : : : : | | | : : : : | | | : : : : | | | : : : : | | | :
QY 418 IWKIRYKRRKQEAVMGKTLISYQPTGYGFKMCAVYLVNGDMGKTHLSLFFVIM 477
:| | | : : : : | | | : : : : | | | : : : : | | | : : : : | | | :
Db 493 SGDNDALEWPNVQNAIMTLDQEDARN 522
:| | | : : : : | | | : : : : | | | : : : : | | | : : : : | | | :
QY 478 RGEYDALLPWFQKQVTLM-LMDQGSRRH 506
:| | | : : : : | | | : : : : | | | : : : : | | | : : : : | | | :

RESULT 12
ENTRY   HYHUMA      #type complete

```

```

TITLE         meprin A (EC 3.4.24.18) alpha chain precursor - human
ALTERNATE_NAMES intestinal brush border metalloendopeptidase;
                  N-benzoyl-L-tyrosyl-p-aminobenzoic acid hydrolase; PABA
                  peptide hydrolase (PPH) alpha chain
ORGANISM      #formal_name Homo sapiens #common_name man
DATE          19-May-1994 #sequence_revision 16-Feb-1996 #text_change
05-Sep-1997
ACCESSIONS    S60193; S39464; S39465; A41196
REFERENCE     S60193
#authors      Eldering, J.A.; Grunberg, J.; Sterchi, E.E.
#submission   submitted to the EMBL Data Library, August 1994
#accession    S60193
#molecule_type mRNA
#residues     1-746 #label ELD
#cross-references EMBL:M82962; NID:G535474; PID:G535475
REFERENCE     S39464
#authors      Dummermuth, E.; Eldering, J.A.; Gruenberg, J.; Jiang, W.;
                  Sterchi, E.E.
#journal      FEBS Lett. (1993) 335:367-375
#title        Cloning of the PABA peptide hydrolase alpha subunit
                  (PPH-alpha) from human small intestine and its expression
                  in COS-1 cells.
#accession    S39464
#molecule_type mRNA
#residues     33-746 #label DUM
#accession    S39465
#molecule_type protein
#residues     66-83 #label DU2
#note         human meprin A alpha chain appears to be expressed in
                  intestine but not in kidney
REFERENCE     A41196
#authors      Dummermuth, E.; Sterchi, E.E.; Jiang, W.; Wolz, R.L.; Bond,
                  J.S.; Flannery, A.V.; Beynon, R.J.
#journal      J. Biol. Chem. (1991) 266:21381-21385
#title        The astacin family of metalloendopeptidases.
#cross-references MIM:92042028
#accession    A41196
#molecule_type mRNA
#residues     65-263 #label DU3
#cross-references GB:M82962; GB:M74238
GENETICS      #gene      GDB:MEPIA
                  #cross-references GDB:371059; OMIM:600388
                  #map_position 6p21.2-6p21.1
COMPLEX       may form homodimers, homotetramers, or heterotetramers with
                  two alpha chains and two beta chains (see HYHUMB)
FUNCTION       zinc metalloproteinase
CLASSIFICATION #superfamily meprin A; astacin homology; EGF homology; MAM
              homology
KEYWORDS       glycoprotein; hydrolase; metalloproteinase; transmembrane
              protein; zinc
FEATURE        #domain signal sequence #status predicted #label SIG\
1-21          #domain propeptide #status predicted #label PRO\
22-65         #product meprin A alpha chain #status predicted #label
              MAT\
66-746        #domain astacin homology #label AST\
75-261        #domain MAM homology #label MAM\
264-433       #domain EGF homology #label EGF\
674-709       #domain transmembrane #status predicted #label TRM\
718-740
107-259,128-147,
674-685,679-694,
696-709
140,222,414,440,
447,539
155,159,165,214
156
SUMMARY       #length 746 #molecular-weight 84367 #checksum 7669
              #length 746; Score 135; DB 1; Length 746;
Query Match

```

Query Match	7.5%; Score 132; DB 1; Length 700;
Best Local Similarity	33.3%; Pred. No. 9.47e-04;
Matches	30; Conservative 20; Mismatches 29; Indels 11; Gaps 7;
Db	431 IWHIRNTQFI-GSPNG-TI--YSPPPYSSK-GYAF--QIYLN---LAHVTNAGIYFHLI 480 ::: : :: : :: :: : ::
Yy	418 IWKIRDYKRRKQEAVMGKTLISLQSPFYGYFGYKMCARYLNGDGKMGKTHLSLFFVIM 477 ::: : :: : :: :: : ::
Db	481 SGANDDOLQWPCPQQATWTLLDQNDPIRQ 510 ::: : :: : :: :: : ::
Yy	478 RGEYDALLPWPFK-QKVTLMMLMDQSSRRH 506 ::: : :: : :: :: : ::
RESULT	14
ENTRY	A60364 #type complete
TITLE	tropomyosin - migratory locust
ORGANISM	#formal_name LOCusta migratoria #common_name migratory locust
DATE	03-Feb-1993 #sequence_revision 03-Feb-1993 #text_change 18-Jun-1993
ACCESSIONS	A60364
REFERENCE	A60364
authors	Krieger, J.; Raming, K.; Knipper, M.; Grau, M.; Mertens, S.; Breer, H.
#journal	Insect Biochem. (1990) 20:173-184
#title	Cloning, sequencing and expression of locust tropomyosin.
#accession	A60364
#status	not compared with conceptual translation
#molecule_type	mRNA
#residues	1-283 #label KRI
CLASSIFICATION	#superfamily tropomyosin
KEYWORDS	coiled coil; heptad repeat
SUMMARY	#length 283 #molecular_weight 32439 #checksum 4917
Query Match	7.3%; Score 128; DB 2; Length 283;
Best Local Similarity	21.3%; Pred. No. 2.90e-03;
Matches	16; Conservative 24; Mismatches 34; Indels 1; Gaps 1;
Db	41 EPARALQKQIOTIENDLQTESLGQVAKLIEEKALONAESEVAALNRRRIQLEEDLE 100 :: ::: : :: ::: : ::: : ::: : ::: : :: ::
Yy	327 EXLKELDKRIEIRPFROWNEA-DSMKSSVESIONRVTLESVDKSGAQARNTGLLESQLS 385 :: ::: : :: ::: : ::: : ::: : ::: : :: ::
Db	101 RSEERLATATAKLAIE 115 :: ::: : :: ::: : ::: : ::: : :: ::
Yy	386 RHQDLSVHDRIAD 400 :: ::: : :: ::: : ::: : ::: : :: ::
RESULT	15
ENTRY	A42908 #type complete
TITLE	meprin A (EC 3.4.24.18) beta chain - rat
ALTERNATE_NAMES	endopeptidase-2 beta chain; meprin beta chain; meprin-a beta chain
ORGANISM	#formal_name Rattus norvegicus #common_name Norway rat
DATE	17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 20-Mar-1998
ACCESSIONS	A42908
REFERENCE	A42908
authors	Johnson, G.D.; Hersh, L.B.
#journal	J. Biol. Chem. (1992) 267:13505-13512
#title	Cloning a rat meprin cDNA reveals the enzyme is a heterodimer.
#cross-references	MUID:92317075
#accession	A42908
#status	preliminary
#molecule_type	mRNA
#residues	1-668 #label JOH
#note	sequence extracted from NCBI backbone (NCBIP:107784)
CLASSIFICATION	#superfamily meprin A; astacin homology; EGF homology; MAM homology
KEYWORDS	heterodimer; hydrolase; metalloproteinase; zinc
FEATURE	#domain astacin homology #label AST\
72-258	#domain MAM homology #label MAM\
261-430	

```

153,157,163,212      #binding_site zinc (His, His, Tyr) #status
                        predicted\
154                  #active_site Glu #status predicted
SUMMARY              #length 668 #molecular-weight 75049 #checksum 9806

Query Match          6.9%   Score 121; DB 2; Length 668;
Best Local Similarity 31.6%; Pred.No. 1.98e-02;
Matches 24; Conservative 19; Mismatches 26; Indels 7; Gaps 5;

Db    441 LLGGQITVTSPPYSSK-GYAF--QINL--D-LTSTNVGLFHLISGDQLQWPCPW 494
QY    432 VMGKTILSLYSQPTVGFGYKMCARYLNCDGNGKGTHTLSLFVIMRGYDALLPWPFK 490
      ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
      |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

Db    495 QQATMTLLDNQNPDRQ 510
QY    491 QKYTLMLMDQGSSRRH 506
      ||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

```

